IFW16

RAW SEQUENCE LISTING   DATE: 09/13/2004
PATENT APPLICATION: US/10/013,036A   TIME: 09:44:53

Input Set : A:\Corrected Seq. Listing.2004.08.31.txt
Output Set: N:\CRF4\09132004\J013036A.raw

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  5 <110> APPLICANT: Hillman, Jeffrey
  9 <120> TITLE OF INVENTION: Antimicrobial Polypeptide, Nucleic Acid, and Methods of Use
 13 <130> FILE REFERENCE: 00-1323H
 15 <140> CURRENT APPLICATION NUMBER: US 10/013,036A
 16 <141> CURRENT FILING DATE: 2001-10-30
 19 <150> PRIOR APPLICATION NUMBER: 09/361,900
 21 <151> PRIOR FILING DATE: 1999-07-27
 25 <150> PRIOR APPLICATION NUMBER: 08/871,924
 27 <151> PRIOR FILING DATE: 1997-06-10
 31 <160> NUMBER OF SEQ ID NOS: 12
 35 <170> SOFTWARE: PatentIn version 3.1
 39 <210> SEQ ID NO: 1
 41 <211> LENGTH: 1316
 43 <212> TYPE: DNA
 45 <213> ORGANISM: Streptococcus mutans
 49 <220> FEATURE:
 51 <221> NAME/KEY: CDS
 53 <222> LOCATION: (796)..(987)
 55 <223> OTHER INFORMATION:
 59 <220> FEATURE:
 61 <221> NAME/KEY: -35_signal
 63 <222> LOCATION: (738)..(742)
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 71 <221> NAME/KEY: -10_signal
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 81 <221> NAME/KEY: RBS
 83 <222> LOCATION: (784)..(791)
 85 <223> OTHER INFORMATION:
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 92 attttttaaaa tttttaaaaa aaattattac ttactttcat gataagtcag tagatatgtc     120
 94 tgaattagaa cattatatta atatagttga agaaataaat cctacgattg cttcaattct     180
 96 taaatctaat ttgaatcagc ttttataaag ttttagccat taaagccatc ttgataaatt     240
 98 ttatatcttt catattcatt aaatgtggag ataatgaaaa agcaacggtt atgctatcgc     300
100 tgcttttttt gtgattagaa gctatgttat catggagtta tagtaatgaa acatagtgac     360
102 agttcatcct ttcttattat aaaagtggta ataagagaag tggtaaacaa agagttagta     420
104 aaataatacg tttaaccata atatttcctc ctttaattta ttataagatt caaaaaggta     480
106 atattcctat atttgcaaat atgggataaa ataattttaa aaaagcagat ttgcaatttt     540
108 aaaaaaatag aggctaatgg tggtattata ttattgtaaa tatatgttta ctcagtaata     600
110 gtgatttact attacaacag attttgttgt tatcttagat atttctgcta gcattagtta     660
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112 tctgtagatg tactacttaa taagtatata attataatta tataataact attatcagat    720
114 taccgttaaa agttttctga tatgcttcta ctgaacaatt tatgttcagt tacacacatg    780
116 aaaaaggagg atatt atg tca aac aca caa tta tta gaa gtc ctt ggt act     831
117                   Met Ser Asn Thr Gln Leu Leu Glu Val Leu Gly Thr
118                   1               5                  10
120 gaa act ttt gat gtt caa gaa gat ctc ttt gct ttt gat aca aca gat     879
121 Glu Thr Phe Asp Val Gln Glu Asp Leu Phe Ala Phe Asp Thr Thr Asp
122         15                  20                  25
124 act act att gtg gca agc aac gac gat cca gat act cgt ttc aaa agt     927
125 Thr Thr Ile Val Ala Ser Asn Asp Asp Pro Asp Thr Arg Phe Lys Ser
126      30                  35                  40
128 tgg agc ctt tgt acg cct ggt tgt gca agg aca ggt agt ttc aat agt     975
129 Trp Ser Leu Cys Thr Pro Gly Cys Ala Arg Thr Gly Ser Phe Asn Ser
130 45                  50                  55                  60
132 tac tgt tgc tga ttgtataaaa gatttagatt gtgccgcatg ttagcggcac        1027
133 Tyr Cys Cys
136 aatcttttga tattagaggt attaatatgt taaatacaca attattagaa gtccttggta   1087
138 ctaaaacttt tgatgttcaa gaagatttat ttgagtttaa tataacagat actattgtac   1147
140 tgcaggctag tgatagtcca gatactcata gtaggggtcc cgagcgctta gtgggaattt   1207
142 gtatcgataa ggggtacaaa ttcccactaa accaatgttt caaggcctat ttattttta    1267
144 tattcaattc tcttaagtgt ttaggaatag ataacaagtc aaatttata              1316
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149 <211> LENGTH: 63
151 <212> TYPE: PRT
153 <213> ORGANISM: Streptococcus mutans
157 <400> SEQUENCE: 2
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160 1               5                  10                  15
163 Val Gln Glu Asp Leu Phe Ala Phe Asp Thr Thr Asp Thr Thr Ile Val
164             20                  25                  30
167 Ala Ser Asn Asp Asp Pro Asp Thr Arg Phe Lys Ser Trp Ser Leu Cys
168          35                  40                  45
171 Thr Pro Gly Cys Ala Arg Thr Gly Ser Phe Asn Ser Tyr Cys Cys
172      50                  55                  60
175 <210> SEQ ID NO: 3
177 <211> LENGTH: 1323
179 <212> TYPE: DNA
181 <213> ORGANISM: Streptococcus mutans
185 <220> FEATURE:
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189 <222> LOCATION: (228)..(782)
191 <223> OTHER INFORMATION:
195 <220> FEATURE:
197 <221> NAME/KEY: -35_signal
199 <222> LOCATION: (177)..(182)
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207 <221> NAME/KEY: -10_signal
209 <222> LOCATION: (191)..(196)
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      228 ttactgttgt taactataaa ttatacttaa attgatagga aacttggtcg tgacattatc     120
      230 atatgttgat attggaagag aatcaaattt ataaagacaa ttaaatctaa atttgatgaa     180
      232 tatttagatg aattattact aggttgacag tcatgttagg agaagag atg aac gat     236
      233                                                     Met Asn Asp
      234                                                     1
      236 ttt caa ttt caa gat tat ttt atg tac aga aaa cca tta ggc aac ttt     284
      237 Phe Gln Phe Gln Asp Tyr Phe Met Tyr Arg Lys Pro Leu Gly Asn Phe
      238     5                   10                  15
      240 tct aat ttt ttt agt ata act gat acg atg gat ccc att gag tta cta     332
      241 Ser Asn Phe Phe Ser Ile Thr Asp Thr Met Asp Pro Ile Glu Leu Leu
      242 20                  25                  30                  35
      244 cat agt gat ccg ata ttt gct gaa gga gta tat ttg gcc tct tca tct     380
      245 His Ser Asp Pro Ile Phe Ala Glu Gly Val Tyr Leu Ala Ser Ser Ser
      246             40                  45                  50
      248 ctt aga gca gcc ata aat aaa ctt aag aat cat act gcg agt act aag     428
      249 Leu Arg Ala Ala Ile Asn Lys Leu Lys Asn His Thr Ala Ser Thr Lys
      250             55                  60                  65
      252 gat aaa aag aat gca aga gag act att ttt caa tac tat gcc cgt tat     476
      253 Asp Lys Lys Asn Ala Arg Glu Thr Ile Phe Gln Tyr Tyr Ala Arg Tyr
      254             70                  75                  80
      256 aac acg aga tca act ccg ttt ggc ttg ttt tcg tcc atc gga gta ggt     524
      257 Asn Thr Arg Ser Thr Pro Phe Gly Leu Phe Ser Ser Ile Gly Val Gly
      258     85                  90                  95
      260 gct ttt tcg gct tac ctt aaa aaa gaa aag tct cgt tat gaa aaa tct     572
      261 Ala Phe Ser Ala Tyr Leu Lys Lys Glu Lys Ser Arg Tyr Glu Lys Ser
      262 100                 105                 110                 115
      264 att aat att gat ctt ttt tgg gct tat aaa gta gca gat aaa cta gaa     620
      265 Ile Asn Ile Asp Leu Phe Trp Ala Tyr Lys Val Ala Asp Lys Leu Glu
      266             120                 125                 130
      268 agt atg cct gaa att tta aat act tta aaa gta gtt gct aat aat gct     668
      269 Ser Met Pro Glu Ile Leu Asn Thr Leu Lys Val Val Ala Asn Asn Ala
      270             135                 140                 145
      272 ttg caa aag tca gat aat ttt tgg ctt ttg gat acg cga agt cat ttt     716
      273 Leu Gln Lys Ser Asp Asn Phe Trp Leu Leu Asp Thr Arg Ser His Phe
      274             150                 155                 160
      276 ggt ctt atg aat tct ttt cat ttt atc ttg tac gac ttc tat tct ttc     764
      277 Gly Leu Met Asn Ser Phe His Phe Ile Leu Tyr Asp Phe Tyr Ser Phe
      278             165                 170                 175
      280 ctt caa gat aga cca taa gaattgatat atcagctgga ttcacaccag     812
      281 Leu Gln Asp Arg Pro
      282 180
      284 aaatacggct agcttgacca atagtttctg ggttaatttt cttaaatttc tgacgtgctt     872
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286 cggtcgcaat agaatcaatg gcatcccaat cgatattctt aggaattcga gctcggtacc    932
288 cggggatcct ctagagtcga cctgcaggca tgcaagcttg gcactggccg tcgttttaca    992
290 acgtcgtgac tgggaaaacc ctggcgttac ccaacttaat cgccttgcag cacatccccc   1052
292 tttcgccagc tggcgtaata gcgaagaggc ccgcaccgat cgcccttccc aacagttgcg   1112
294 cagcctgaat ggcgaatggc gcctgatgcg gtattttctc cttacgcatc tgtgcggtat   1172
296 ttcacaccgc atatggtgca ctctcagtac aatctgctct gatgccgcat agttaagcca   1232
298 gccccgacac ccgccaacac ccgctgacgc gccctgacgg gcttgtctgc tcccggcatc   1292
300 cgcttacaga caagctgtga ccgtctccgg g                                  1323
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305 <211> LENGTH: 184
307 <212> TYPE: PRT
309 <213> ORGANISM: Streptococcus mutans
313 <400> SEQUENCE: 4
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319 Gly Asn Phe Ser Asn Phe Phe Ser Ile Thr Asp Thr Met Asp Pro Ile
320   20   25   30
323 Glu Leu Leu His Ser Asp Pro Ile Phe Ala Glu Gly Val Tyr Leu Ala
324   35   40   45
327 Ser Ser Ser Leu Arg Ala Ala Ile Asn Lys Leu Lys Asn His Thr Ala
328   50   55   60
331 Ser Thr Lys Asp Lys Lys Asn Ala Arg Glu Thr Ile Phe Gln Tyr Tyr
332 65   70   75   80
335 Ala Arg Tyr Asn Thr Arg Ser Thr Pro Phe Gly Leu Phe Ser Ser Ile
336   85   90   95
339 Gly Val Gly Ala Phe Ser Ala Tyr Leu Lys Lys Glu Lys Ser Arg Tyr
340   100   105   110
343 Glu Lys Ser Ile Asn Ile Asp Leu Phe Trp Ala Tyr Lys Val Ala Asp
344   115   120   125
347 Lys Leu Glu Ser Met Pro Glu Ile Leu Asn Thr Leu Lys Val Val Ala
348   130   135   140
351 Asn Asn Ala Leu Gln Lys Ser Asp Asn Phe Trp Leu Leu Asp Thr Arg
352 145   150   155   160
355 Ser His Phe Gly Leu Met Asn Ser Phe His Phe Ile Leu Tyr Asp Phe
356   165   170   175
359 Tyr Ser Phe Leu Gln Asp Arg Pro
360   180
363 <210> SEQ ID NO: 5
365 <211> LENGTH: 22
367 <212> TYPE: PRT
369 <213> ORGANISM: Streptococcus mutans
373 <220> FEATURE:
375 <221> NAME/KEY: MISC_FEATURE
377 <222> LOCATION: (3)..(3)
379 <223> OTHER INFORMATION: 2,3-didehydroalanine
383 <220> FEATURE:
385 <221> NAME/KEY: MISC_FEATURE
387 <222> LOCATION: (5)..(5)
389 <223> OTHER INFORMATION: alanyl moiety of lanthionine

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393 <220> FEATURE:
395 <221> NAME/KEY: MISC_FEATURE
397 <222> LOCATION: (7)..(7)
399 <223> OTHER INFORMATION: alanyl moiety of lanthionine
403 <220> FEATURE:
405 <221> NAME/KEY: MISC_FEATURE
407 <222> LOCATION: (11)..(11)
409 <223> OTHER INFORMATION: alanyl moiety of lanthionine
413 <220> FEATURE:
415 <221> NAME/KEY: MISC_FEATURE
417 <222> LOCATION: (16)..(16)
419 <223> OTHER INFORMATION: alanyl moiety of lanthionine
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425 <221> NAME/KEY: MISC_FEATURE
427 <222> LOCATION: (19)..(19)
429 <223> OTHER INFORMATION: alanyl moiety of lanthionine
433 <220> FEATURE:
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437 <222> LOCATION: (21)..(21)
439 <223> OTHER INFORMATION: alanyl moiety of lanthionine
443 <220> FEATURE:
445 <221> NAME/KEY: MISC_FEATURE
447 <222> LOCATION: (8)..(8)
449 <223> OTHER INFORMATION: 2,3-didehydrobutyrine
453 <220> FEATURE:
455 <221> NAME/KEY: MISC_FEATURE
457 <222> LOCATION: (14)..(14)
459 <223> OTHER INFORMATION: S-2-aminobutyric acid
463 <220> FEATURE:
465 <221> NAME/KEY: MISC_FEATURE
467 <222> LOCATION: (22)..(22)
469 <223> OTHER INFORMATION: S-[aminovinyl]-cysteine
473 <220> FEATURE:
475 <221> NAME/KEY: THIOETH
477 <222> LOCATION: (5)..(7)
479 <223> OTHER INFORMATION:
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489 <223> OTHER INFORMATION:
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509 <223> OTHER INFORMATION:
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 09/13/2004
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Input Set : **A:\Corrected Seq. Listing.2004.08.31.txt**
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<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 3,5,7,8,11,14,16,19,21,22
Seq#:6; Xaa Pos. 3,5,7,8,11,14,16,19,21,22
Seq#:7; Xaa Pos. 3,5,7,8,11,14,16,19,21,22
Seq#:8; Xaa Pos. 3,5,7,8,11,14,16,19,21,22
Seq#:9; Xaa Pos. 3,5,7,8,11,14,16,19,21,22
Seq#:10; Xaa Pos. 3,5,7,8,11,14,16,19,21,22
Seq#:11; Xaa Pos. 3,5,7,8,11,14,16,19,21,22

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Input Set : **A:\Corrected Seq. Listing.2004.08.31.txt**
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L:89 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:85
L:205 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:191
L:215 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:201
L:225 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:211
L:225 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:221
L:493 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:479
L:503 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:489
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L:513 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:509
L:515 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
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L:653 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:639
L:663 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:649
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L:813 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:799
L:823 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:809
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L:833 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:829
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L:993 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:989
L:995 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
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L:1443 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:1429
L:1453 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:1439
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L:1479 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:16